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GenCore version 4.5

QM protein - protein search, using SW model

Ran on: August 21, 2002, 15:44:28 : Search time 13:43 seconds
 (without alignments)

Perfect score: 1778
 Sequence: 1 M Q A V D N L T S A P G N T I S L C T R I S Q D N R K K E W i u g G D P N E T P M 342
 986.008 Million cell updates/sec

Scoring Table: BLOSUM62
 Gapop 10.0 , Gapext: 0.5

Searched: 105224 seqs, 38719550 residues

Minimum DB seq length: 0

Post-processing: Maximum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SWISSPROT_40.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	772	43.4	338	K101_HUMAN
2	694	39.0	305	K101_RAT
3	488	27.4	319	H263_HUMAN
4	411.5	23.1	375	G97K_MOUSE
5	409.5	23.0	381	G97K_HUMAN
6	394	22.2	342	P49505_HUMAN
7	392.5	22.1	342	P49505_CAVIA
8	379.5	21.3	361	EB12_HUMAN
9	367	20.6	345	C172_PIG
10	366	20.6	341	P49505_MOUSE
11	362	20.4	341	P49505_RAT
12	357.5	20.1	308	P2Y5_CHICK
13	347.5	19.5	1	C172_HUMAN
14	347	19.5	537	P287_XENLA
15	344	19.3	309	C172_MOUSE
16	339	19.1	1	C172_RAT
17	339	19.1	359	AG2R_BOVIN
18	338	19.0	344	P2Y5_HUMAN
19	334	18.8	1	AG2R_SHEEP
20	329.5	18.5	339	GPRH_HUMAN
21	329	18.5	1	AG2B_HUMAN
22	328	18.4	340	C171_PIG
23	327	18.4	1	AG2R_PIG
24	326	18.3	359	AG2B_CANFA
25	325.5	18.3	1	PAR2_MOUSE
26	325	18.3	359	1 AG2R_RABBIT
27	321	18.1	359	1 AG2R_HUMAN
28	320	18.0	1	AG2R_CAVPO
29	320	18.0	370	1 P2Y9_HUMAN
30	319.5	18.0	365	P49505_HUMAN
31	319	17.7	359	1 AG2R_RAT
32	319	17.7	1	AG2S_MOUSE
33	319	17.9	359	1 AG2R_MOUSE

SUMMARIES

ALIGNMENTS					
RESULT	1	K101_HUMAN	STANDARD;	PRT:	338 AA.
ID	K101_HUMAN				
AC	Q15391;				
DT	15-JUL-1998 (Rel. 36, Created)				
DT	15-JUL-1998 (Rel. 36, Last sequence update)				
DT	30-MAY-2000 (Rel. 39, Last annotation update)				
DE	Probable G protein-coupled receptor KIAA0001.				
GN	KIAA0001.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE: Bone marrow;				
RX	MEDLINE-96051387; PubMed-7584026;				
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,				
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Takata S.;				
RT	*Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1*;				
RT	DNA Res. 1:27-35(1994).				
RL	DR: EMBL: D13626; RAA02791.1; -.				
CC	DR: GCRDB; GCR_0594; -.				
CC	DR: InterPro; IPR002276; SPCR_Rhodopsin.				
CC	DR: Pfam; PF00001; 7m_1; 1.				
CC	DR: PROSITE; PS00337; G_PROTEIN_RECV_F1_1; FALSE_NEG.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).				
FT	TRANSMEM 30 50 1 (POTENTIAL).				
FT	DOMAIN 51 55 CYTOSOLIC (POTENTIAL).				
FT	TRANSMEM 55 76 2 (POTENTIAL).				
FT	DOMAIN 77 96 EXTRACELLULAR (POTENTIAL).				
FT	TRANSMEM 97 117 3 (POTENTIAL).				
FT	DOMAIN 118 139 CYTOSOLIC (POTENTIAL).				
FT	TRANSMEM 140 160 4 (POTENTIAL).				
FT	DOMAIN 161 188 EXTRACELLULAR (POTENTIAL).				
FT	TRANSMEM 189 209 5 (POTENTIAL).				
FT	DOMAIN 210 234 CYTOSOLIC (POTENTIAL).				
FT	TRANSMEM 235 255 6 (POTENTIAL).				
PRO	34 316.5 17.8 359 1 ORGANIC MOLECULES				
PRO	35 316 17.8 359 1 AGES_MOUSE				
PRO	36 316 17.8 377 1 APJ-RAT				
PRO	37 313.5 17.6 380 1 APJ_HUMAN				
PRO	39 313.5 17.6 401 1 OPRM_PTG				
PRO	40 312 17.5 359 1 AG2R_MEUN				
PRO	41 312 17.5 401 1 OPRM_BOVIN				
PRO	42 311 17.5 369 1 PAR1_MOUSE				
PRO	43 310.5 17.5 393 1 AG2R_XENIA				
PRO	44 310.5 17.5 393 1 AG2S_XENIA				
PRO	45 310 17.4 374 1 PAR3_HUMAN				
PRO	000254 homo sapien				

